

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/786,501

Source: _____

Date Processed by STIC: _____

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/786,501

DATE: 12/03/2004

TIME: 07:11:26

Input Set : N:\Crf3\RULE60\10786501.raw.txt

Output Set: N:\CRF4\12032004\J786501.raw

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1 <110> APPLICANT: Acton, Susan
2 <120> TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
3 <130> FILE REFERENCE: MNI-050
4 <140> CURRENT APPLICATION NUMBER: US/10/786,501
5 <141> CURRENT FILING DATE: 2004-02-25
6 <150> PRIOR APPLICATION NUMBER: US/09/757,982
7 <151> PRIOR FILING DATE: 2001-01-10
8 <150> PRIOR APPLICATION NUMBER: 09/163,115
9 <151> PRIOR FILING DATE: 1998-09-29
10 <160> NUMBER OF SEQ ID NOS: 15
11 <170> SOFTWARE: PatentIn Ver. 2.0
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 4137
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapiens
17 <220> FEATURE:
18 <223> OTHER INFORMATION: 'n' at positions 2872, 3597 and 3682 may be any nucleic acid
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W--> 20 <222> LOCATION: (297)..(1202)
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23      actccggacg cgctcgcag tgcgcagggt gggcgccccg cgctgcagc gtccgccggg 120
24      gcggcgccgc gggaggtggc cgacaggctc cgggcctcgc agcctcagcc cccggcccag 180
25      cgcgctttcc gacggcgggc ccgcgcggag ccacccgccc gcccaaggtc tctcgcgggc 240
26      ggggaaacgg aaaactccca acttcctgag ttctaaagtt cctgttgctt cagaca atg 299
27                                     Met
28                                     1
29      gat gag caa tca caa gga atg caa ggg cca cct gtt cct cag ttc caa 347
30      Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe Gln
31          5                      10                      15
32      cca cag aag gcc tta cga ccg gat atg ggc tat aat aca tta gcc aac 395
33      Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala Asn
34          20                      25                      30
35      ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt tat 443
36      Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr
37          35                      40                      45
38      aga gca gcc tgt ctc ttg gat gga gta cca gta gct tta aaa aaa gtg 491
39      Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys Val
40          50                      55                      60                      65
41      cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc aaa 539
42      Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile Lys
43          70                      75                      80
44      gaa ata gat ctt ctt aag caa ctc aac cat cca aat gta ata aaa tat 587

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45   Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys Tyr
46           85                      90                      95
47   tat gca tca ttc att gaa gat aat gaa cta aac ata gtt ttg gaa cta 635
48   Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu
49           100                      105                      110
50   gca gat gct ggc gac cta tcc aga atg atc aag cat ttt aag aag caa 683
51   Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys Gln
52           115                      120                      125
53   aag agg cta att cct gaa aga act gtt tgg aag tat ttt gtt cag ctt 731
54   Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu
55           130                      135                      140                      145
56   tgc agt gca ttg gaa cac atg cat tct cga aga gtc atg cat aga gat 779
57   Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg Asp
58           150                      155                      160
59   ata aaa cca gct aat gtg ttc att aca gcc act ggg gtg gta aaa ctt 827
60   Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu
61           165                      170                      175
62   gga gat ctt ggg ctt ggc cgg ttt ttc agc tca aaa acc aca gct gca 875
63   Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala Ala
64           180                      185                      190
65   cat tct tta gtt ggt acg cct tat tac atg tct cca gag aga ata cat 923
66   His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His
67           195                      200                      205
68   gaa aat gga tac aac ttc aaa tct gac atc tgg tct ctt ggc tgt cta 971
69   Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu
70           210                      215                      220                      225
71   cta tat gag atg gct gca tta caa agt cct ttc tat ggt gac aaa atg 1019
72   Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met
73           230                      235                      240
74   aat tta tac tca ctg tgt aag aag ata gaa cag tgt gac tac cca cct 1067
75   Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro
76           245                      250                      255
77   ctt cct tca gat cac tat tca gaa gaa ctc cga cag tta gtt aat atg 1115
78   Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Met
79           260                      265                      270
80   tgc atc aac cca gat cca gag aag cga cca gac gtc acc tat gtt tat 1163
81   Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val Tyr
82           275                      280                      285
83   gac gta gca aag agg atg cat gca tgc act gca agc agc taaacatgca 1212
84   Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser
85           290                      295                      300
86   agatcatgaa gagtgtaacc aaagtaattg aaagtatttt gtgcaaagtc gtacctscoc 1272
87   atttatgtct ggggtgtaag attaataatt cagagctagt gtgctctgaa tccttaacca 1332
88   gttttcatat aagcttcatt ttgtaccagt cacctaaatc acctccttgc aacccccaaa 1392
89   tgactttgga ataactgaat tgcattgttag gagagaaaat gaaacatgat ggttttgaat 1452
90   ggctaaagggt ttatagaatt tcttacagtt ttctgctgat aaattgtgtt tagatagact 1512
91   gtcagtgcca aatattgaag gtgcagcttg gcacacatca gaatagactc atacctgaga 1572
92   aaaagtatct gaacatgtga cttgtttctt ttttagtaat ttatggacat tgagatgaac 1632
93   acaattgtga acttttgtga agattttatt tttaaacggt tgaagtacta gttttagttc 1692

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94      ttagcagagt agttttcaaa tatgattctt atgataaatg tagacacaaa ctatttgaga 1752
95      aacattttaga actccttagct tatacattca aaatgtaact attaaatgtg aagatttggg 1812
96      gacaaaatgt gagtcagaca ctgaagagtt ttttgttttg ttttaatat tttgatattc 1872
97      tctttgcatt gaaatggat aaatgaatcc atttaaaaag tgggttaagga tttggtttagc 1932
98      tgggtgtgata ataattttta aagttgcaca ttgcccaagg ctttttttgt gtgtttttat 1992
99      tgttggttgt acatttgaaa aatattcttt gaataacctt gcagtactat atttcaagrt 2052
100     ttctttataa atttaagtgc attttaactc ataattgtac actataatat aagcctaagt 2112
101     ttttattcat aagttttatt gaagttctga tgggtccctc tcagaaattt ttttatatta 2172
102     ttcttcaagt tactttctta tttatattgt atgtgcattt tatccattaa tgtttcatac 2232
103     tttctgagag tataataccc ttttaaaaga tatttggtat accaatactt ttcttgga 2292
104     gaaaactttt tttaaacttt ttaaaatttg ggccactctg tatgcatatg tttggtcttg 2352
105     ttaagagga agaaaggatg tgtgttatac tgtacctgtg aatgttgata cagttacaat 2412
106     ttatttgaca aggttgtaat tctagaatat gcttaataaa atgaaaactg gccatgacta 2472
107     cagccagaac tgttatgaga ttaacatttc tattgagaag cttttgagta aagtactgta 2532
108     tttgttcatg aagatgactg agatggtaac acttcgtgta gcttaaggaa atgggcagaa 2592
109     tttcgtaaat gctgttggtg agatgtgttt tccctgaatg ctttcgtatt agtggcgacc 2652
110     agtttctcac agaattgtga agcctgaagg ccaagaggaa gtcactgtta aaggactctg 2712
111     tgccatctta caaccttgga tgaattatcc tgccaacgtg aaaacctcat gttcaaagaa 2772
112     cacttccctt tagccgatgt aactgctggt tttgtttttc atatgtgttt ttcttacact 2832
W--> 113     catttgaatg ctttcaagca tttgtaaact taaaaaaaa wawaaagggc aaaaagtctg 2892
114     aaccttggtt ttctgaaatc taatcagtta tgtatggttt ctgaagggtg attttatttt 2952
115     ggaataggta aagcgaaacc tgttttctcw tgttttctc gagggctaga tgcatttttt 3012
116     ttctcacact cttaatgact tttaacattt atactgagca tccatagata tattcctaga 3072
117     agtatgagaa gaattattct tattgacct taatgtcatg ttcattttaa tgtaataata 3132
118     ttgagatgaa atgttctctg gttggaacag atactctctt ttttttctt gcaatcttta 3192
119     agaatacata gatctaaaat tcattagctt gacccctcaa agtaactttt aagtaaagat 3252
120     taaagctttt cttctcagtg aatatactg ctagaaggaa atagctggga agaatttaat 3312
121     gatcagggaa attcattatt tctatatgtg gaaacttttt gcttcgaata ttgtatcttt 3372
122     ttaaatctaa atgttcatat ttttctgaa gaaaccactg tgtaaaaaatc aaattttaat 3432
123     tttgaatgga ataatttcaa agaactatga agatgatttg aagctctaatt ttatatagtc 3492
124     acctataaaa tgttctttat atgtgttcat aagtaaaattt tatattgatt aagttaaact 3552
125     tttgaattga tttgaggagc agtaaaatga aagctatata tattnctaaa ccytatttag 3612
126     acattggkac cagttaccca ggtgaaaata kggagtaact ttgttttgta tggtaagggt 3672
127     taggaatggn ggatgaaggg tatctctata taaataaagt gctcaacaat gtgcaatgat 3732
128     tgtaaattta gtaagatatt acagccattt catgaatgct ttaccattca acatagtatc 3792
129     tattacaaaa cacctttctt gtatccatat acttcagggt ttgctgttaa catttactat 3852
130     gatattttatt ttaacaaaaa tgttactcac attaaatggt tattctttaa aatgaatgta 3912
131     ttatgttttt aaccacaaaa tgcatactta cctgtgcct catatttcaa tagtactgta 3972
132     atatggacat cttttgtgaa atacttttat tttgttatgc tttaaatata cataaaaaa 4032
133     gatttctgtt attagctttg aaaattgtat aatatcctaa tataacaaaa atataaaaa 4092
134     aaaaatgaat acagtaaaaa aaaaaaaaaa aaaaaaaaaa aaagg 4137
136 <210> SEQ ID NO: 2
137 <211> LENGTH: 302
138 <212> TYPE: PRT
139 <213> ORGANISM: Homo sapiens
140 <400> SEQUENCE: 2
141     Met Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe
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143     Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala

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Input Set : N:\Crif3\RULE60\10786501.raw.txt

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144          20          25          30
145  Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val
146          35          40          45
147  Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys
148          50          55          60
149  Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile
150          65          70          75          80
151  Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys
152          85          90          95
153  Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu
154          100          105          110
155  Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys
156          115          120          125
157  Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln
158          130          135          140
159  Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg
160          145          150          155          160
161  Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys
162          165          170          175
163  Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala
164          180          185          190
165  Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile
166          195          200          205
167  His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys
168          210          215          220
169  Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys
170          225          230          235          240
171  Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro
172          245          250          255
173  Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn
174          260          265          270
175  Met Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val
176          275          280          285
177  Tyr Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser
178          290          295          300
180 <210> SEQ ID NO: 3
181 <211> LENGTH: 906
182 <212> TYPE: DNA
183 <213> ORGANISM: Homo sapiens
184 <220> FEATURE:
185 <221> NAME/KEY: CDS
186 <222> LOCATION: (1)..(906)
187 <400> SEQUENCE: 3
188  atg gat gag caa tca caa gga atg caa ggg cca cct gtt cct cag ttc 48
189  Met Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe
190      1          5          10          15
191  caa cca cag aag gcc tta cga ccg gat atg ggc tat aat aca tta gcc 96
192  Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala
193          20          25          30

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194	aac ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt	144
195	Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val	
196	35 40 45	
197	tat aga gca gcc tgt ctc ttg gat gga gta cca gta gct tta aaa aaa	192
198	Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys	
199	50 55 60	
200	gtg cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc	240
201	Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile	
202	65 70 75 80	
203	aaa gaa ata gat ctt ctt aag caa ctc aac cat cca aat gta ata aaa	288
204	Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys	
205	85 90 95	
206	tat tat gca tca ttc att gaa gat aat gaa cta aac ata gtt ttg gaa	336
207	Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu	
208	100 105 110	
209	cta gca gat gct ggc gac cta tcc aga atg atc aag cat ttt aag aag	384
210	Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys	
211	115 120 125	
212	caa aag agg cta att cct gaa aga act gtt tgg aag tat ttt gtt cag	432
213	Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln	
214	130 135 140	
215	ctt tgc agt gca ttg gaa cac atg cat tct cga aga gtc atg cat aga	480
216	Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg	
217	145 150 155 160	
218	gat ata aaa cca gct aat gtg ttc att aca gcc act ggg gtg gta aaa	528
219	Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys	
220	165 170 175	
221	ctt gga gat ctt ggg ctt ggc cgg ttt ttc agc tca aaa acc aca gct	576
222	Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala	
223	180 185 190	
224	gca cat tct tta gtt ggt acg cct tat tac atg tct cca gag aga ata	624
225	Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile	
226	195 200 205	
227	cat gaa aat gga tac aac ttc aaa tct gac atc tgg tct ctt ggc tgt	672
228	His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys	
229	210 215 220	
230	cta cta tat gag atg gct gca tta caa agt cct ttc tat ggt gac aaa	720
231	Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys	
232	225 230 235 240	
233	atg aat tta tac tca ctg tgt aag aag ata gaa cag tgt gac tac cca	768
234	Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro	
235	245 250 255	
236	cct ctt cct tca gat cac tat tca gaa gaa ctc cga cag tta gtt aat	816
237	Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn	
238	260 265 270	
239	atg tgc atc aac cca gat cca gag aag cga cca gac gtc acc tat gtt	864
240	Met Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val	
241	275 280 285	
242	tat gac gta gca aag agg atg cat gca tgc act gca agc agc	906

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 2872,3597,3682

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 2,18

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10786501.raw.txt

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L:19 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!

L:20 M:281 W: Numeric Fields not Ordered, <222> Sort in ascending order!

L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2832

M:341 Repeated in SeqNo=1